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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/087,190	02/28/2002	Pia M. Challita-Eid	511582003420	7796
36327 7590 07/20/2007 AGENSYS C/O MORRISON & FOERSTER LLP 12531 HIGH BLUFF DRIVE SUITE 100 SAN DIEGO, CA 92130-2040			EXAMINER	
			BLANCHARD, DAVID J	
			ART UNIT	PAPER NUMBER
			1643	
			•	
			MAIL DATE	DELIVERY MODE
•			07/20/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

	Application No.	Applicant(s)			
·	10/087,190	CHALLITA-EID ET AL.			
Office Action Summary	Examiner	Art Unit			
•	David J. Blanchard	1643			
The MAILING DATE of this communication app Period for Reply	ears on the cover sheet with the	correspondence address			
A SHORTENED STATUTORY PERIOD FOR REPLY WHICHEVER IS LONGER, FROM THE MAILING DA - Extensions of time may be available under the provisions of 37 CFR 1.13 after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory period versiture to reply within the set or extended period for reply will, by statute, Any reply received by the Office later than three months after the mailing earned patent term adjustment. See 37 CFR 1.704(b).	ATE OF THIS COMMUNICATION 36(a). In no event, however, may a reply be the vill apply and will expire SIX (6) MONTHS from a cause the application to become ABANDON	N. imely filed m the mailing date of this communication. ED (35 U.S.C. § 133).			
Status					
	Responsive to communication(s) filed on <u>04 April 2007</u> .				
,	,—				
,	Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under <i>Ex parte Quayle</i> , 1935 C.D. 11, 453 O.G. 213.				
closed in accordance with the practice under E	x parte Quayle, 1935 G.D. 11, 2	153 O.G. 213.			
Disposition of Claims					
4) Claim(s) 83,86 and 87 is/are pending in the application.					
4a) Of the above claim(s) <u>86 and 87</u> is/are withdrawn from consideration.					
5) Claim(s) is/are allowed.	1				
6)⊠ Claim(s) <u>83</u> is/are rejected.					
7) Claim(s) is/are objected to.	r clastian requirement				
8) Claim(s) are subject to restriction and/o	r election requirement.				
Application Papers					
9) The specification is objected to by the Examine	r.				
10)☐ The drawing(s) filed on is/are: a)☐ accepted or b)☐ objected to by the Examiner.					
Applicant may not request that any objection to the					
Replacement drawing sheet(s) including the correct 11) The oath or declaration is objected to by the Ex	- ·				
Priority under 35 U.S.C. § 119		•			
12) Acknowledgment is made of a claim for foreign a) All b) Some * c) None of:	priority under 35 U.S.C. § 119(a)-(d) or (f).			
1. Certified copies of the priority documents have been received.					
2. Certified copies of the priority documents have been received in Application No					
3. Copies of the certified copies of the prior	•	ved in this National Stage			
application from the International Bureau	, , , ,				
* See the attached detailed Office action for a list	or the certified copies not receive	rea.			
Attachment(s)		·			
Notice of References Cited (PTO-892) Notice of Draftsperson's Patent Drawing Review (PTO-948)	4) Interview Summa Paper No(s)/Mail				
3) Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date 6/28/07.		Patent Application			

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DETAILED ACTION

1. Claims 83 and 86-87 are pending.

Claims 1-82, 84-85 and 88-110 are cancelled.

Claims 83 and 86-87 have been amended.

- 2. Claims 86-87 remain withdrawn from further consideration by the Examiner, 37 C.F.R. § 1.142(b) as being drawn to a nonelected invention.
- 3. Claim 83 is under consideration to the extent that the transcript variant encodes the protein of SEQ ID NO:5, i.e., applicants' elected species.
- 4. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Objections/Rejections Withdrawn

- 5. The objection to applicants' benefit claim on the fist line of the specification, the incomplete address of the ATCC (e.g., pg. 63, lines 7-8) and the use of trademarks have been withdrawn in view of the amendments made to the newly submitted substitute specification filed 4/4/2007.
- 6. The substitute specification has been entered in full.
- 7. The replacement drawings filed 4/4/2007 have been entered in full.
- 8. The rejection of claims 83-85 under 35 U.S.C. 112, second paragraph, as being indefinite in the recitation "121P1F1 gene (SEQ ID NO:1)" in claim 83 is withdrawn in view of the cancellation of claims 84-85 and the amendments to claim 83.
- 9. The rejection of claims 83-84 under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention is withdrawn in view of the cancellation of claim 84 and the amendments to claim 83.
- 10. The rejection of claim 84 under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated 121P1F1 transcript or transcripts that

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encode the protein of SEQ ID NO:2, does not reasonably provide enablement for: (i) any isolated 121P1F1 transcript variant that encodes a protein comprising at least one amino acid substitution, addition or deletion relative to SEQ ID NO:2 or the transcript variant of SEQ ID NO:5 is withdrawn in view of the cancellation of claim 84.

11. The rejection of claims 83-84 under 35 U.S.C. 102(e) as being anticipated by Tang et al (US Patent 6,569,662, filed 7/19/2000) is withdrawn in view of the cancellation of claim 84 and the amendments to claim 83.

Rejections Maintained

12. The rejection of claim 83 under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated 121P1F1 transcript or transcripts that encode the protein of SEQ ID NO:2, does not reasonably provide enablement for: (i) any isolated 121P1F1 transcript variant that encodes a protein comprising at least one amino acid substitution, addition or deletion relative to SEQ ID NO:2 or the transcript variant of SEQ ID NO:5 is maintained.

The response filed 4/4/2007 acknowledges the issue pertaining to variants that contain an amino acid substitution, addition or deletion relative to SEQ ID NO:2 and states that this language has been removed from the claims. Applicant states that the claims now recite particular variants. Applicants' arguments have been fully considered but are not found persuasive for reasons of record. While applicant has deleted the claim language "comprising at least one amino acid substitution, addition or deletion relative to SEQ ID NO:2", the claims remain drawn to a transcript variant encoding the protein of SEQ ID NO:5 (i.e., applicants' elected species). Thus, while the claims are not broad in scope, the present application does not provide sufficient enablement for a transcript variant encoding the protein of SEQ ID NO:5 for reasons already of record.

Applicant discloses an isolated 121P1F1 protein of SEQ ID NO:2 that is encoded by a nucleotide sequence of SEQ ID NO:1 that is highly expressed in prostate cancer and a method of producing said protein in the instant specification. Applicant has not

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taught how to make and/or use (i) any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant, or (ii) the structural and functional characteristics of any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant.

Applicant has not provided sufficient biochemical information (e.g. structural characteristics, amino acid composition, physicochemical properties, etc) that distinctly identifies (i) any isolated 121P1F1-related protein or any fragment of said protein inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant, or (ii) the structural and functional characteristics of any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant. The specification does not provide sufficient guidance as to which isolated 121P1F1-related protein or any fragment of said protein would share the same function as the 121P1F1 protein of SEQ ID NO:2.

Neither does the specification provide any working examples of any 121P1F1-related protein (i.e., SEQ ID NO:5) that have the same functional activities or characteristics, i.e., highly expressed in prostate cancer as the 121P1F1 protein.

It is reiterated that Attwood (Science 2000; 290:471-473, of record) teaches that "[i]t is presumptuous to make functional assignments merely on the basis of some degree of similarity between sequences. Similarly, Skolnick et al. (Trends in Biotech. 2000; 18(1):34-39, of record) teach that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2). Finally, even single amino acid differences can result in drastically altered functions between two proteins. For example, Metzler et al. (Nature Structural Biol. 1997; 4:527-531, of record) show that any of a variety of single amino acid changes can alter or

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abolish the ability of CTLA4 to interact with its ligands CD80 and CD86 (e.g., summarized in Table 2). Thus it is unpredictable if any functional activity will be shared by two polypeptides having less than 100% identity over the full length of their sequences.

In view of this unpredictability; the skilled artisan would not reasonably expect a polypeptide (i.e., SEQ ID NO:5) having anything less than 100% identity *over the full length of SEQ ID NO:2* to *share the same function, if known,* as the 121P1F1 protein having the amino acid sequence of SEQ ID NO:2. For example, an antibody epitope may be as small as 6-15 shared amino acid residues (e.g., Lerner Nature 1982; 299:592-596, see page 595-596, of record) and places no limitations on the function of the protein containing the polypeptide sequence recognized. Thus, there is insufficient guidance and direction to assist the skilled artisan to make and use (i) any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant, or (ii) the structural and functional characteristics of any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant without undue experimentation.

Protein chemistry is probably one of the most unpredictable areas of biotechnology. It is known in the art that even single amino acid changes or differences in a proteins amino acid sequence can have dramatic effects on the protein's function. For example, Mikayama et al. (PNAS, 1993. 90: 10056-10060, of record) teach that the human glycosylation factor (GIF) protein differs from human macrophage migration inhibitory factor (MIF) by a single amino acid residue (see Figure 1 in particular). Yet, Mikayama et al. further teach that GIF is unable to carry out the function of MIF and MIF does not demonstrate GIF activity (see Abstract in particular). Burgess et al (J Cell Biol. 111:2129-2138, 1990, of record) show that a conservative replacement of a single "lysine" reside at position 118 of acidic fibroblast growth factor by "glutamic acid" led to the substantial loss of heparin binding, receptor binding and biological activity of the protein. Similarly, Lazar et al. (Mol Cell Biol. 8:1247-1252, 1988, of record) teach that in transforming growth factor alpha, replacement of aspartic acid at position 47 with

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alanine or asparagines did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen. These references demonstrate that even a single amino acid substitution or what appears to be an inconsequential chemical modification will often dramatically affect the biological activity and characteristic of a protein. Furthermore, the specification fails to teach what deletions, truncations, substitutions and mutations of the disclosed sequence can be tolerated that will allow the protein to function as the protein of SEQ ID NO:2, if known. While it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with reasonable expectation of success are limited. Certain positions in the sequence are critical to the three-dimensional structure/function relationship, and these regions can tolerate only conservative substitutions or no substitutions. Applicant has not provided sufficient guidance to enable one skill in the art to use (i) any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant, or (ii) the structural and functional characteristics of any isolated 121P1F1-related protein or any fragment of said protein, inclusive to the protein of SEQ ID NO:5 encoded by the presently claimed transcript variant.

In view of the quantity of experimentation necessary, the unpredictability of the art, the lack of sufficient guidance in the specification, the absence of working examples, and the limited amount of direction provided, it would take undue experimentation to practice the claimed invention.

- 13. No claims are allowed.
- 14. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not

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mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David J. Blanchard whose telephone number is (571) 272-0827. The examiner can normally be reached at Monday through Friday from 8:00 AM to 6:00 PM, with alternate Fridays off. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Larry Helms, can be reached at (571) 272-0832.

The official fax number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/David J. Blanchard/ Primary Examiner, A.U. 1643